

# SEQUENCE LISTING

<110> Walke, D. Wade  
Turner, C. Alexander Jr.  
Abuin, Alejandro  
Friedrich, Glenn  
Zambrowicz, Brian  
Sands, Arthur T.

<120> Novel Human Proteases and  
Polynucleotides Encoding the Same

<130> LEX-0108-USA

<150> US 60/171,566

<151> 1999-12-22

<160> 7

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 921

<212> DNA

<213> Homo sapiens

<400> 1

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| tttgaacrag  | gtaaatctgc  | arctctttcg | ctcccaaaag | ctcccagttg  | tgggcagagt | 120 |
| ctgggttaagg | tacagccttg  | gaattatttt | aacattttca | gtcgcattct  | tggaggaagc | 180 |
| caagtggaga  | agggttccta  | tccctggcag | gtatctctga | aacaaaaggca | gaagcatatt | 240 |
| tgtggaggaa  | gcatacgtctc | accacagtgg | gtgatcacgg | cggctcactg  | cattgcaaac | 300 |
| agaaacattg  | tgtctacttt  | gaatgttact | gctggagagt | atgacttaag  | ccagacagac | 360 |
| ccaggagagc  | aaactctcac  | tattgaaact | gtcatcatac | atccacattt  | ctccaccaag | 420 |
| aaaccaatgg  | actatgatat  | tgcccttttg | aagatggctg | gagccttcca  | atttggccac | 480 |
| tttgtggggc  | ccatatgtct  | tccagagctg | cgggagcaat | ttgaggctgg  | ttttatttgt | 540 |
| acaactgcag  | gctggggccg  | cttaactgaa | ggtggcgtcc | tctcacaagt  | cttgaggaa  | 600 |
| gtgaatctgc  | ctattttgac  | ctgggaagag | tgtgtggcag | ctctgttaac  | actaaagagg | 660 |
| cccatcagtg  | ggaagacctt  | tctttgcaca | ggttttcctg | atggaggagg  | agacgcattg | 720 |
| caggagagatt | caggagggtc  | actcatgtgc | cggaataaga | aaggggcctg  | gactctggct | 780 |
| ggtgtgactt  | cctgggggtt  | gggctgtggt | cgaggctgga | gaaacaatgt  | gaggaaaagt | 840 |
| gatcaaggat  | cccctgggat  | cttcacagac | attagtaaag | tgctttcctg  | gatccacgaa | 900 |
| cacatccaaa  | ctggttaacta | a          |            |             |            | 921 |

<210> 2

<211> 306

<212> PRT

<213> Homo sapiens

<400> 2

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Leu | Lys | Met | Leu | Ile | Ser | Arg | Asn | Lys | Leu | Ile | Leu | Leu | Leu |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Gly | Ile | Val | Phe | Glu | Arg | Gly | Lys | Ser | Ala | Ala | Leu | Ser | Leu | Pro |     |
|     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |     |     |
| Lys | Ala | Pro | Ser | Cys | Gly | Gln | Ser | Leu | Val | Lys | Val | Gln | Pro | Trp | Asn |



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900  
909

<210> 4  
<211> 302  
<212> PRT  
<213> Homo sapiens

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1 5 10 15  
Phe Glu Arg Gly Lys Ser Ala Ala Leu Ser Leu Pro Lys Ala Pro Ser  
20 25 30  
Cys Gly Gln Ser Leu Val Lys Val Gln Pro Trp Asn Tyr Phe Asn Ile  
35 40 45  
Phe Ser Arg Ile Leu Gly Gly Ser Gln Val Glu Lys Gly Ser Tyr Pro  
50 55 60  
Trp Gln Val Ser Leu Lys Gln Arg Gln Lys His Ile Cys Gly Gly Ser  
65 70 75 80  
Ile Val Ser Pro Gln Trp Val Ile Thr Ala His Cys Ile Ala Asn  
85 90 95  
Arg Asn Ile Val Ser Thr Leu Asn Val Thr Ala Gly Glu Tyr Asp Leu  
100 105 110  
Ser Gln Thr Asp Pro Gly Glu Gln Thr Leu Thr Ile Glu Thr Val Ile  
115 120 125  
Ile His Pro His Phe Ser Thr Lys Lys Pro Met Asp Tyr Asp Ile Ala  
130 135 140  
Leu Leu Lys Met Ala Gly Ala Phe Gln Phe Gly His Phe Val Gly Pro  
145 150 155 160  
Ile Cys Leu Pro Glu Leu Arg Glu Gln Phe Glu Ala Gly Phe Ile Cys  
165 170 175  
Thr Thr Ala Gly Trp Gly Arg Leu Thr Glu Gly Gly Val Leu Ser Gln  
180 185 190  
Val Leu Gln Glu Val Asn Leu Pro Ile Leu Thr Trp Glu Glu Cys Val  
195 200 205  
Ala Ala Leu Leu Thr Leu Lys Arg Pro Ile Ser Gly Lys Thr Phe Leu  
210 215 220  
Cys Thr Gly Phe Pro Asp Gly Gly Arg Asp Ala Cys Gln Gly Asp Ser  
225 230 235 240  
Gly Gly Ser Leu Met Cys Arg Asn Lys Lys Gly Ala Trp Thr Leu Ala  
245 250 255  
Gly Val Thr Ser Trp Gly Leu Gly Cys Gly Arg Gly Trp Arg Asn Asn  
260 265 270  
Val Arg Lys Ser Asp Gln Gly Ser Pro Gly Ile Phe Thr Asp Ile Ser  
275 280 285  
Lys Val Leu Ser Trp Ile His Glu His Ile Gln Thr Gly Asn  
290 295 300

<210> 5  
<211> 495  
<212> DNA  
<213> Homo sapiens

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60  
120

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gcaggctggg gccgcttaac tgaaggtggc gtcctctcac aagtcttgca ggaagtgaat 180
ctgcctatatt tgacctggga agagtgtgtg gcagctctgt taacctataa gagggccatc 240
agtgggaaga cctttctttg cacaggtttt cctgatggag ggagagacgc atgtcaggga 300
gattcaggag gttcactcat gtgccggaat aagaaagggg cctggactct ggctgggtgtg 360
acttcctggg gtttgggctg tggctcaggc tggagaaaca atgtgaggaa aagtgatcaa 420
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caaactggta actaa 495

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<210> 6  
 <211> 164  
 <212> PRT  
 <213> Homo sapiens

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<400> 6
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Gly His Phe Val Gly Pro Ile Cys Leu Pro Glu Leu Arg Glu Gln Phe
          20          25          30
Glu Ala Gly Phe Ile Cys Thr Thr Ala Gly Trp Gly Arg Leu Thr Glu
          35          40          45
Gly Gly Val Leu Ser Gln Val Leu Gln Glu Val Asn Leu Pro Ile Leu
          50          55          60
Thr Trp Glu Glu Cys Val Ala Ala Leu Leu Thr Leu Lys Arg Pro Ile
          65          70          75          80
Ser Gly Lys Thr Phe Leu Cys Thr Gly Phe Pro Asp Gly Gly Arg Asp
          85          90          95
Ala Cys Gln Gly Asp Ser Gly Gly Ser Leu Met Cys Arg Asn Lys Lys
          100          105          110
Gly Ala Trp Thr Leu Ala Gly Val Thr Ser Trp Gly Leu Gly Cys Gly
          115          120          125
Arg Gly Trp Arg Asn Asn Val Arg Lys Ser Asp Gln Gly Ser Pro Gly
          130          135          140
Ile Phe Thr Asp Ile Ser Lys Val Leu Ser Trp Ile His Glu His Ile
          145          150          155          160
Gln Thr Gly Asn

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<210> 7  
 <211> 1568  
 <212> DNA  
 <213> Homo sapiens

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ttccattttca ggtgtcgtga aaagcttgaa ttcggcgcgc cagatatcac acgtgccaag 180
ggactggctc aaaggcttcc tatttttgtt tgcttttagtc tctctaaaat ttcagggaaa 240
aactatgagt ctcaaaatgc ttataagcag gaacaagctg attttactac taggaatagt 300
cttttttgaa craggtaaatt ctgcacctct ttcgctcccc aaagctccca gttgtgggca 360
gagtctggtt aaggtacagc cttggaatta ttttaacatt ttcagtcgca ttcttgagg 420
aagccaagtg gagaagggtt cctatccctg gcaggatatc ctgaaacaaa ggcagaagca 480
tatttgtgga ggaagcatcg tctcaccaca gtgggtgatc acggcggctc actgcattgc 540
aaacagaaac atttgttcta ctttgaatgt tactgctgga gagtatgact taagccagac 600
agaccagga gagcaaactc tcactattga aactgtcatc atacatccac atttctccac 660
caagaaacca atggactatg atattgccct tttgaagatg gctggagcct tccaatttgg 720
ccactttgtg gggcccatat gtcttccaga gctgcgggag caatttgagg ctggttttat 780

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